

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Malcolm Whitman and Xin Chen

5 (ii) TITLE OF THE INVENTION: METHODS AND REAGENTS FOR MODULATING
TGF-BETA SUPERFAMILY SIGNALLING

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Clark & Elbing LLP
- (B) STREET: 176 Federal Street
- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02110

10 (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

15 (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 27-MAY-1998
- (C) CLASSIFICATION:

20 (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/047,991
- (B) FILING DATE: 28-MAY-1997

25 (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Bieker-Brady, Kristina
- (B) REGISTRATION NUMBER: 39,109
- (C) REFERENCE/DOCKET NUMBER: 00246/501002

30 (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-428-0200
- (B) TELEFAX: 617-428-7045
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
5 (D) OTHER INFORMATION: Xenopus Smad2 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGTCGTCCA	TCTTGCCTTT	CACCCCGCCA	GTAGTGAAGC	GCCTGCTAGG	ATGGAAGAAG	60
TCTGCAAGTG	GCACCAACAGG	AGCAGGTGGC	GATGAGCAGA	ACGGACAGGA	AGAGAAGTGG	120
10 TCGAAAAAG	CGGTAAGAG	CTTGGTAAA	AAACTGAAGA	AAACGGGACA	ATTAGACGAG	180
CTTGAGAAGG	CGATCACGAC	GCAGAACTGC	AACACGAAAT	GCGTAACGAT	ACCAAGCAGT	240
TGCTCTGAAA	TTTGGGGACT	GAGTACAGCA	AATACCATAG	ATCAGTGGGA	TACCACAGGC	300
CTTTACAGCT	TCTCTGAACA	AACCAGGTCT	CTTGATGGTC	GACTCCAGGT	GTCTCACCGT	360
AAAGGATTGC	CGCATGTTAT	CTACTGCAGA	CTGTGGCCT	GGCCAGACCT	GCACAGTCAT	420
15 CATGAACCTGA	AAGCAATCGA	AAATTGTGAA	TATGCTTTA	ACCTAAAAAA	AGATGAAGTT	480
TGTGTCAATC	CATACCAATT	TCAGAGGGTG	GAGACACCAG	TTTACCCACC	TGTATTAGTT	540
CCACGGCACA	CGGAAATCTT	GACAGAGCTG	CCACCTCTG	ATGACTACAC	GCATTCCATT	600
CCAGAAAACA	CTAATTTC	TGCAGGGATT	GAACCTCAGA	GCAATTATAT	TCCAGAAACA	660
20 CCACCTCTG	GATATATTAG	TGAAGATGGA	GAAACTAGCG	ATCAGCAACT	TAACCAAAGC	720
ATGGACACAG	GGTCACCAGC	TGAGCTGTCT	CCGAGTACAC	TTTCTCCAGT	CAACCACAAT	780
CTCGATTTC	AACCTGTAC	CTATTGGAA	CCTGCTTTT	GGTGCCTCTAT	AGCATACTAC	840
GAACTGAATC	AGCGAGTAGG	AGAAAACCTTC	CATGCATCGC	AACCACCGCT	TACCGTGGAC	900
GGCTTTACGG	ACCCCTCAA	CTCTGAAAGG	TTCTGCTTAG	TTTACTCTC	AAATGTGAAAC	960
25 CGAAATGCA	CGGTGAAAT	GACCAGCGT	CACATAGAA	GGGGTGTCCG	GCTATATTAC	1020
ATCGGTGGAG	AGGTGTTGC	AGAGTGCCTA	AGTGATAGTG	CTATTTTGT	TCAGAGTCCA	1080
AACTGTAAACC	AGCGATATGG	ATGGCATCCA	GCAACTGTAT	GTAAGATTCC	TCCAGGATGC	1140
AATCTGAAGA	TTTTCAATAA	TCAAGAGTTT	GCGGCTCTCC	TCGCTCAGTC	TGTGAATCAA	1200
GGCTTTGAAG	CAGTTTATCA	GTTAACCTGA	ATGTGCACCA	TAAGGATGAG	CTTGTAAAAA	1260
30 GGCTGGGGTG	CTGAATACAG	GGCACAGACCC	GTTACAAGCA	CTCCATGCTG	GATTGAGCTT	1320
CACCTGAATG	GACCTTGCA	GTGGTTGGAC	AAAGTGTGA	CACAGATGGG	ATCCCCTTCA	1380
GTCCGCTGCT	CAAGCATGTC	CTAATGGCT	CCTCTTTTA	ATGTATTACC	TGCGGGCGGC	1440
AACTGCAGTC	CCAGCAACAG	ACTCAATACA	GCTTGTCTGT	CGTAGTATTT	GTGTGTGGTG	1500
CCCATGAACT	GTTTACAATC	CAAAAGAGAG	AGAATAAAA	AGCAAAAAACA	GCACTTGAGA	1560
TCCCATCAAC	GAAAAGCACC	TTGTTGGATG	ATGTTCTGA	TACTCTAAA	GTAGATCCGT	1620
35 GTATAAATGA	CTCCTTACCT	GGGAAAAGGG	ACTTTTC			1658

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
45 (D) OTHER INFORMATION: Xenopus Smad2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu		
1	5	10	15
5	Gly Trp Lys Lys Ser Ala Ser Gly Thr Thr Gly Ala Gly Gly Asp Glu		
	20	25	30
	Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu		
	35	40	45
10	Val Lys Lys Leu Lys Lys Thr Gly Gln Leu Asp Glu Leu Glu Lys Ala		
	50	55	60
	Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr		
65	70	75	80
	Cys Ser Glu Ile Trp Gly Leu Ser Thr Ala Asn Thr Ile Asp Gln Trp		
	85	90	95
15	Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp		
	100	105	110
	Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr		
	115	120	125
	Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys		
20	130	135	140
	Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val		
145	150	155	160
	Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro		
	165	170	175
25	Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro		
	180	185	190
	Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala		
195	200	205	
	Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly		
	210	215	220
30	Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser		
225	230	235	240
	Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Ser Thr Leu Ser Pro		
	245	250	255
35	Val Asn His Asn Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala		
	260	265	270
	Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu		
275	280	285	
	Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp		
290	295	300	
40	Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn		
305	310	315	320
	Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val		
	325	330	335
45	Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp		
	340	345	350
	Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp		
355	360	365	
	His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile		
370	375	380	
50	Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln		
385	390	395	400
	Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met		
	405	410	415

Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr
 420 425 430
 Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp
 435 440 445
 5 Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser
 450 455 460
 Ser Met Ser
 465

(2) INFORMATION FOR SEQ ID NO:3:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xenopus Smad2 MH2 domain

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr
 1 5 10 15
 Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro
 20 25 30
 25 Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
 35 40 45
 Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg
 50 55 60
 30 Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
 65 70 75 80
 Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
 85 90 95
 35 Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
 100 105 110
 Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
 115 120 125
 Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
 130 135 140
 40 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
 145 150 155 160
 Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
 165 170 175
 45 Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser
 180 185 190
 Met Ser

(2) INFORMATION FOR SEQ ID NO:4:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

15 (A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Human Smad2 coding region

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15	ATGTCGTCCA TCTTGCCTT CACGCCGCCA GTTGTGAAGA GACTGCTGGG ATGGAAGAAG	60
	TCAGCTGGTG GGTCTGGAGG AGCAGGCCGA GGAGAGCAGA ATGGCCAGGA AGAAAAGTGG	120
	TGTGAGAAAG CAGTGAAAG TCTGGTGAAG AAGCTAAAGA AAACAGGACG ATTAGATGAG	180
	CTTGAGAAAG CCATCACCCAC TCAAAACTGT AATACTAAAT GTGTTACCAT ACCAACGACT	240
	TGCTCTGAAA TTTGGGGACT GAGTACACCA AATACGATAG ATCAGTGGGA TACAACAGGC	300
	CTTTACAGCT TCTCTGAACA ACCCAGGTCT CTTGATGGTC GTCTCCAGGT ATCCCATCGA	360
20	AAAGGATTGC CACATGTTAT ATATTGCCGA TTATGGCGCT GGCCTGATCT TCACAGTCAT	420
	CATGAACCTCA AGGCAATTGA AACTGCGAA TATGCTTTA ATCTTAAAAA GGATGAAGTA	480
	TGTGTAAACC CTTACCACTA TCAGAGAGTT GAGACACCAG TTTTGCCTCC AGTATTAGTG	540
	CCCCGACACA CCGAGATCCT AACAGAACTT CCGCCTCTGG ATGACTATAC TCACTCCATT	600
	CCAGAAAACA CTAACCTCCC AGCAGGAATT GAGCCACAGA GTAATTATAT TCCAGAAACG	660
25	CCACCTCTG GATATATCAG TGAAGATGGA GAAACAAGTG ACCAACAGTT GAATCAAAGT	720
	ATGGACACAG GCTCTCCAGC AGAACTATCT CCTACTACTC TTTCCCTGT TAATCATAGC	780
	TTGGATTTCAG AGCCAGTTAC TTACTCAGAA CCTGCATTTT GGTGTTCAAT AGCATATTAT	840
	GAATTAAATC AGAGGGTTGG AGAAACCTTC CATGCATCAC AGCCCTCACT CACTGTAGAT	900
	GGCTTTACAG ACCCATCAA TTCAGAGAGG TTCTGCTTAG GTTACTCTC CAATGTTAAC	960
30	CGAAATGCCA CGGTAGAAAT GACAAGAAGG CATATAGGAA GAGGAGTGC CTTATACTAC	1020
	ATAGGTGGGG AAGTTTTGTC TGAGTGCCTA AGTGATAGTG CAATCTTTGT GCAGAGCCCC	1080
	AATTGTAATC AGAGATATGG CTGGCACCT GCAACAGTGT GTAAAATTCC ACCAGGCTGT	1140
	AATCTGAAGA TCTTCAACAA CCAGGAATT GCTGCTCTTC TGGCTCAGTC TGTTAACAG	1200
	GGTTTTGAAG CCGCTCTATCA GCTAACTAGA ATGTGCACCA TAAGAATGAG TTTTGTGAAA	1260
35	GGGTGGGGAG CAGAATACCG AAGGCAGACG GTAACAAGTA CTCCTTGCTG GATTGAACCTT	1320
	CATCTGAATG GACCTCTACA GTGGTTGGAC AAAGTATTAA CTCAGATGGG ATCCCTTCA	1380
	GTGCGTTGCT CAAGCATGTC A	1401

40 (2) INFORMATION FOR SEQ ID NO:5:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Human Smad2

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
 1 5 10 15
 Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Glu
 20 25 30
 10 Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
 35 40 45
 Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala
 50 55 60
 Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr
 65 70 75 80
 Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp
 85 90 95
 Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp
 100 105 110
 20 Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr
 115 120 125
 Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys
 130 135 140
 Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val
 145 150 155 160
 Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro
 165 170 175
 Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro
 180 185 190
 30 Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala
 195 200 205
 Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly
 210 215 220
 Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser
 225 230 235 240
 35 Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro
 245 250 255
 Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala
 260 265 270
 40 Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu
 275 280 285
 Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp
 290 295 300
 45 Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn
 305 310 315 320
 Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val
 325 330 335
 Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp
 340 345 350
 50 Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp
 355 360 365
 His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile

370	375	380
Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln		
385	390	395
Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met		
5 405	410	415
Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr		
420	425	430
Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp		
435	440	445
10 Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser		
450	455	460
Ser Met Ser		
465		

(2) INFORMATION FOR SEQ ID NO:6:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human Smad2 MH2 domain

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr	1 5 10 15	
Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro		
30 20 25 30		
Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg		
35 35 40 45		
Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg		
50 50 55 60		
Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser		
35 65 70 75 80		
Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Trp His		
85 85 90 95		
Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe		
40 100 105 110		
Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly		
115 115 120 125		
Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser		
130 130 135 140		
45 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser		
145 145 150 155 160		
Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu		
165 165 170 175		

Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser
 180 185 190
 Met Ser

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1272

(D) OTHER INFORMATION:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Human Smad3 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG TCG TCC ATC CTG CCT TTC ACT CCC CCG ATC GTG AAG CGC CTG CTG	48
Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu	
1 5 10 15	
GGC TGG AAG AAG GGC GAG CAG AAC GGG CAG GAG GAG AAA TGG TGC GAG	96
Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu	
20 25 30	
AAG GCG GTC AAG AGC CTG GTC AAG AAA CTC AAG AAG ACG GGG CAG CTG	144
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Thr Gly Gln Leu	
30 35 40 45	
GAC GAG CTG GAG AAG GCC ATC ACC ACG CAG AAC GTC AAC ACC AAG TGC	192
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys	
50 55 60	
ATC ACC ATC CCC AGG TCC CTG GAT GGC CGG TTG CAG GTG TCC CAT CGG	240
Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg	
65 70 75 80	
AAG GGG CTC CCT CAT GTC ATC TAC TGC CCT GTG CGA TGG CCA GAC CTG	288
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu	
85 90 95	
CAC AGC CAC CAC GAG CTG CGG GCC ATG GAG CTG TGT GAG TTC GCC TTC	336
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe	

	100 ~	105	110	
	AAT ATG AAG AAG GAC GAG GTC GTG AAT CCC TAC CAC TAC CAG AGA Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln Arg 115	120	125	384
5	GTA GAG ACA CCA GTT CTA CCT CCT GTG TTG GTG CCA CGC CAC ACA GAG Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr Glu 130	135	140	432
	ATC CCG GCC GAG TTC CCC CCA CTG GAC GAC TAC AGC CAT TCC ATC CCC Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile Pro 145	150	155	480
10	GAA AAC ACT AAC TTC CCC GCA GGC ATC GAG CCC CAG AGC AAT ATT CCA Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile Pro 165	170	175	528
	GAG ACC CCA CCC CCT GGC TAC CTG AGT GAA GAT GGA GAA ACC AGT GAC Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser Asp 180	185	190	576
15	CAC CAG ATG AAC CAC AGC ATG GAC GCA GGT TCT CCA AAC CTA TCC CCG His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser Pro 195	200	205	624
	AAT CCG ATG TCC CCA GCA CAT AAT AAC TTG GAC CTG CAG CCA GTT ACC Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val Thr 210	215	220	672
20	TAC TGC GAG CCG GCC TTC TGG TGC TCC ATC TCC TAC TAC GAG CTG AAC Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn 225	230	235	720
	CAG CGC GTC GGG GAG ACA TTC CAC GCC TCG CAG CCA TCC ATG ACT GTG Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr Val 245	250	255	768
25	GAT GGC TTC ACC GAC CCC TCC AAT TCG GAG CGC TTC TGC CTA GGG CTG Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu 260	265	270	816
	CTC TCC AAT GTC AAC AGG AAT GCA GCA GTG GAG CTG ACA CGG AGA CAC Leu Ser Asn Val Asn Arg Asn Ala Ala Val Glu Leu Thr Arg Arg His 275	280	285	864
30	ATC GGA AGA GGC GTG CGG CTC TAC TAC ATC GGA GGG GAG GTC TTC GCA Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala 290	295	300	912
	GAG TGC CTC AGT GAC AGC GCT ATT TTT GTC CAG TCT CCC AAC TGT AAC Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn 305	310	315	960
35				
40				

	CAG CGC TAT GGC TGG CAC CCG GCC ACC GTC TGC AAG ATC CCA CCA GGA Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly 325 330 335	1008
5	TGC AAC CTG AAG ATC TTC AAC AAC CAG GAG TTC GCT GCC CTC CTG GCC Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala 340 345 350	1056
	CAG TCG GTC AAC CAG GGC TTT GAG GCT GTC TAC CAG TTG ACC CGA ATG Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met 355 360 365	1104
10	TGC ACC ATC CGC ATG AGC TTC GTC AAA GGC TGG GGA GCG GAG TAC AGG Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg 370 375 380	1152
15	AGA CAG ACT GTG ACC AGT ACC CCC TGC TGG ATT GAG CTG CAC CTG AAT Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn 385 390 395 400	1200
	GGG CCT TTG CAG TGG CTT GAC AAG GTC CTC ACC CAG ATG GGC TCC CCA Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro 405 410 415	1248
20	AGC ATC CGC TGT TCC AGT GTG TCT TAGAGACATC AAGTATGGTA GGGGAGGGCA Ser Ile Arg Cys Ser Ser Val Ser 420	1302
25	GGCTTGGGA AAATGCCAT ACAGGAGGTG GAGAAAATTG GAACTCTACT CAACCCATTG TTGTCAAGGA AGAAGAAATC TTCTCCCTC AACTGAAGGG GTGCACCCAC CTGTTTCTG AAACACACGA GCAAAACCCAG AGGTGGATGT TATGAACAGC TGTGTCTGCC AAACACATT ACCCCTTGGC CCCACTTGA AGGGCAAGAA ATGGCGTCTG CTCTGGTGGC TTAAGTGAGC AGAACAGGTA GTATTACACC ACCGGCACCC TCCCCCCCAGA CTCTTTTTT GAGTGACAGC TTTCTGGGAT GTCACAGTCC AACCAAGAAAC GCCCCCTCTGT CTAGGACTGC AGTGTGGAGT TCACCTTGGA AGGGCGTTCT AGGTAGGAAG AGCCCCGCACG ATGCAGACCT CATGCCAGC TCTCTGACCG TTGTGACAGT GCCTCTTCCA GTGAACATTC CCAGCCCCAGC CCCGGCCCCGT 1362 1422 1482 1542 1602 1662 1722 1782 1842 1902 1962 2022 2082 2142 2202 2234	
30	TGTGAGCTGG ATAGACTTGG GATGGGGAGG GAGGGAGTTT TGTCTGTCTC CCTCCCCCTCT CAGAACATAC TGATTGGGAG GTGCGTGTTC AGCAGAACCT GCACACAGGA CAGCAGGAAA AATCGATGAG CGCCACCTCT TAAAAAAACTC ACTTACGTTG TCCTTTTCA CTTTGAAAAG TTGGAAGGAGC TGCTGAGGAGC CAGTGCATAT GCAATGTATA GTGTCATATTA TCACATTAAT CTCAAAGAGA TTCGAATGAC GGTAAAGTGT CTCATGAAGC AGGAGGCCCT TGTGCGTGGGA 35 TGGCATTTGG TCTCAGGCAG CACCACACTG GGTGCGTCTC CAGTCATCTG TAAGAGCTTG CTCCAGATTG TGATGCATAC GGCTATATTG GTTTATGTAG TCAGTTGCAT TCATTAATC AACTTTATCA TATGCTCAAA AAAAAAAAAG	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 424 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad3

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu
1 5 10 15
Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu
10 20 25 30
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu
35 40 45
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys
50 55 60
15 Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg
65 70 75 80
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu
85 90 95
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe
100 105 110
Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln Arg
115 120 125
Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr Glu
130 135 140
25 Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile Pro
145 150 155 160
Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile Pro
165 170 175
Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser Asp
180 185 190
His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser Pro
195 200 205
Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val Thr
210 215 220
30 Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn
225 230 235 240
Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr Val
245 250 255
Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu
40 260 265 270
Leu Ser Asn Val Asn Arg Asn Ala Ala Val Glu Leu Thr Arg Arg His
275 280 285
Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala
290 295 300
45 Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn
305 310 315 320
Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly
325 330 335
50 Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala
340 345 350
Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met

355 360 365
 Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg
 370 375 380
 Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn
 385 390 395 400
 Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro
 405 410 415
 Ser Ile Arg Cys Ser Ser Val Ser
 420

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human Smad3 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr
 1 5 10 15
 Phe His Ala Ser Gln Pro Ser Met Thr Val Asp Gly Phe Thr Asp Pro
 20 25 30
 Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
 35 40 45
 Asn Ala Ala Val Glu Leu Thr Arg Arg His Ile Gly Arg Gly Val Arg
 50 55 60
 Leu Tyr Tyr Ile Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
 65 70 75 80
 Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
 85 90 95
 35 Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
 100 105 110
 Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
 115 120 125
 40 Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
 130 135 140
 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
 145 150 155 160
 Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
 165 170 175
 45 Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Ile Arg Cys Ser Ser
 180 185 190
 Val Ser

(2) INFORMATION FOR SEQ ID NO:10:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

15 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1554

(D) OTHER INFORMATION:

20 (A) NAME/KEY: Other

(B) LOCATION: 1...1

15 (D) OTHER INFORMATION: Xenopus FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20	ATG AGA GAC CCC TCC AGT CTG TAC TCA GGA TTC CCA GCT GGA TCC CAG Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln 1 5 10 15	48
25	TAT GAA AGT GTG GAG CCT CCC AGC CTT GCC CTG CTG AGC TCT ATA GAC Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp 20 25 30	96
30	CAG GAG CAG CTC CCA GTG GCC ACC GGC CAG TCC TAT AAT CAC AGT GTC Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val 35 40 45	144
35	CAG CCT TGG CCC CAA CCT TGG CCA CCC TTG TCC CTG TAC AGA GAG GGG Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly 50 55 60	192
40	GGC ACG TGG AGC CCA GAC AGA GGC AGT ATG TAT GGA CTC TCC CCC GGC Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly 65 70 75 80	240
45	ACC CAC GAG GGC TCC TGC ACC CAC ACT CAC GAG GGC CCC AAG GAC TCA Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser 85 90 95	288
50	ATG GCA GGA GAC CAG ACC AGG TCC AGG AAG AGC AAA AAG AAG AAT TAT Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr 100 105 110	336
55	CAT CGA TAT AAC AAG CCC CCC TAT TCC TAC CTG GCT ATG ATT GCC CTG His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu 115 120 125	384

	GTC ATC CAG AAC TCG CCC GAG AAG AGG CTC AAA CTC TCC CAG ATC CTG Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu 130 135 140	432
5	AAG GAG GTC AGT ACA CTC TTC CCC TTC TTT AAT GGG GAT TAT ATG GGT Lys Glu Val Ser Thr Leu Phe Pro Phe Asn Gly Asp Tyr Met Gly 145 150 155 160	480
	TGG AAA GAC TCC ATC AGG CAC AAC TTG TCT TCC AGT GAC TGC TTT AAG Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Asp Cys Phe Lys 165 170 175	528
10	AAG ATT CTC AAA GAC CCT GGA AAG CCC CAG GCC AAG GGT AAC TTC TGG Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp 180 185 190	576
15	ACG GTG GAT GTT AGC CGG ATT CCT CTG GAT GCG ATG AAG CTG CAG AAC Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn 195 200 205	624
	ACT GCG TTG ACC CGA GGT GGA TCA GAC TAC TTT GTC CAG GAT TTG GCT Thr Ala Leu Thr Arg Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala 210 215 220	672
20	CCA TAC ATC CTA CAT AAC TAT AAA TAT GAG CAC AAT GCA GGG GCG TAT Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr 225 230 235 240	720
	GGT CAC CAG ATG CCT CCA AGT CAT GCC AGA TCC CTG TCT TTG GCA GAG Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu 245 250 255	768
25	GAC TCT CAA CAG ACC AAC ACT GGT GGC AAA CTT AAC ACA TCC TTT ATG Asp Ser Gln Gln Thr Asn Thr Gly Lys Leu Asn Thr Ser Phe Met 260 265 270	816
30	ATT GAT TCC CTA CTC CAT GAC CTG CAA GAG GTG GAT CTG CCT GAT GCC Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala 275 280 285	864
	TCC AGG AAC CTT GAG AAC CAA AGG ATC TCT CCG GCT GTA GCC ATG AAC Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn 290 295 300	912
35	AAT ATG TGG AGC CCT GCT CCT CTT CTC TAC ACT CAT TCC AAG CCA ACA Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr 305 310 315 320	960
	AGG AAT GCC AGA AGC CCT GGT TTG TCC ACC ATC C A T TCC ACG TAC TCC Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser 325 330 335	1008
40	TCT TCC AGC TCC AGC ATT TCT ACA ATC TCC CCC GTT GGG TTT CAG AAG Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys	1056

	340	345	350	
	GAG CAG GAG AAA AGT GGT CGA CAA ACT CAA AGG GTT GGC CAT CCC ATT			1104
	Glu	Gln	Glu	Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile
	355	360	365	
5	AAA CGA TCA AGA GAG GAC GAT GAC TGC AGT ACC ACA TCT TCA GAT CCT			1152
	Lys	Arg	Ser	Arg Glu Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro
	370	375	380	
	GAC ACT GGG AAC TAC TCT CCC ATT GAG CCC CCA AAG AAG ATG CCC TTG			1200
	Asp	Thr	Gly	Asn Tyr Ser Pro Ile Glu Pro Pro Lys Lys Met Pro Leu
10	385	390	395	400
	CTT TCA TTG GAC TTG CCC ACT TCT TAC ACA AAG AGT GTG GCA CCT AAT			1248
	Leu	Ser	Leu	Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn
	405	410	415	
15	GTA GTG GCA CCA CCA AGT GTC CTG CCC TTC TTT CAT TTT CCT CGC TTC			1296
	Val	Val	Ala	Pro Pro Ser Val Leu Pro Phe Phe His Phe Pro Arg Phe
	420	425	430	
	ACC TAC TAT AAT TAT GGA CCT TCA CCC TAC ATG ACC CCA CCA TAC TGG			1344
	Thr	Tyr	Tyr	Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp
	435	440	445	
20	GGT TTT CCA CAT CCT ACA AAT TCT GGT GGG GAT AGT CCA CGT GGA CCC			1392
	Gly	Phe	Pro	His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro
	450	455	460	
25	CAA TCT CCT CTG GAC CTA GAC AAC ATG TTA CGG GCC ATG CCA CCC AAC			1440
	Gln	Ser	Pro	Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn
	465	470	475	480
	AAG AGT GTG TTT GAT GTG TTG ACA AGT CAC CCA GGT GAC CTC GTC CAT			1488
	Lys	Ser	Val	Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His
	485	490	495	
30	CCG TCC TTC CTC AGT CAA TGC TTG GGC AGC AGT GGT TCC CCG TAC CCA			1536
	Pro	Ser	Phe	Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro
	500	505	510	
	AGC AGA CAA GGC CTT ATG TAGAGACGGA GGCCTCCTGG CCTGACCTGG AGTGGACA			1592
	Ser	Arg	Gln	Gly Leu Met
	515			
35	CTCAATGAAA TGA			1605

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

40

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

✓ (ix) FEATURE:

(A) NAME/KEY: Other

5 (B) LOCATION: 1...1

(D) OTHER INFORMATION: Xenopus FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10 Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln
1 5 10 15
Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp
20 25 30
Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val
35 40 45
15 Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly
50 55 60
Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly
65 70 75 80
Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser
85 90 95
20 Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Asn Tyr
100 105 110
His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu
115 120 125
25 Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu
130 135 140
Lys Glu Val Ser Thr Leu Phe Pro Phe Asn Gly Asp Tyr Met Gly
145 150 155 160
Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys
165 170 175
30 Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp
180 185 190
Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn
195 200 205
35 Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala
210 215 220
Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr
225 230 235 240
Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu
245 250 255
40 Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met
260 265 270
Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala
275 280 285
45 Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn
290 295 300
Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr
305 310 315 320
50 Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser
325 330 335

Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys
 340 345 350
 Glu Gln Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile
 355 360 365
 5 Lys Arg Ser Arg Glu Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro
 370 375 380
 Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro Lys Met Pro Leu
 385 390 395 400
 Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn
 10 405 410 415
 Val Val Ala Pro Pro Ser Val Leu Pro Phe His Phe Pro Arg Phe
 420 425 430
 Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp
 435 440 445
 15 Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro
 450 455 460
 Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn
 465 470 475 480
 Lys Ser Val Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His
 20 485 490 495
 Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro
 500 505 510
 Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro Pro Gly Leu Thr Trp
 515 520 525
 25 Ser Gly His Ser Met Lys
 530

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xenopus FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Ser Ser Asp Pro Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro
 40 1 5 10 15
 Lys Lys Met Pro Leu Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys
 20 25 30
 Ser Val Ala Pro Asn Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe
 35 40 45
 45 His Phe Pro Arg Phe Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met
 50 55 60
 Thr Pro Pro Tyr Trp Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp
 65 70 75 80

Ser Pro Arg Gly Pro Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg
 85 90 95
 Ala Met Pro Pro Asn Lys Ser Val Phe Asp Val Leu Thr Ser His Pro
 100 105 110
 5 Gly Asp Leu Val His Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser
 115 120 125
 Gly Ser Pro Tyr Pro Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro
 130 135 140
 Pro Gly Leu Thr Trp Ser Gly His Ser Met Lys
 10 145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1

(D) OTHER INFORMATION: Human FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25	ATGGGGCCCT GCAGCGGCTC CCGCCTGGGG CCCCCAGAGG CTGAGTCGCC CTCCCAGCCC CCTAAGAGGA GGAAGAAGAG GTACCTGCGA CATGACAAGC CCCCCTACAC CTACTTGCC	60 120
	ATGATCGCCT TGGTGATTCA GGGCGCTCCC TCCCGCAGAC TGAAGCTGGC CCAGATCATC CGTCAGGTCC AGGCGGTGTT CCCCTTCTTC AGGGAAGACT ACGAGGGCTG GAAAGACTCC	180 240
	ATTGCCACA ACCTTTCCTC CAACCGATGC TTCCGCAAGG TGCCAAGGA CCCTGCAAAG CCCCCAGGCCA AGGGCAACTT CTGGGCGGTC GACGTGAGCC TGATCCCAGC TGAGGCGCTC	300 360
30	CGGCTGCAGA ACACCCGCCT GTGCCGGCGC TGGCAGAACG GAGGTGCGCG TGGAGCCTTC GCCAAGGACC TGGGCCCTA CGTGCTGCAC GGCGGCCAT ACCGGCGCC CAGTCCCCCG	420 480
	CCACCAACCA GTGAGGGCTT CAGCATCAAG TCCCTGCTAA GAAGGTCCCG GGAAGGGGCA CCCTGGCCGG GGCTAGCTCC ACAGAACAGC CCAGTTCTG CAGGCACAGG GAACAATGGG	540 600
	GAAGAAGCGG TGCCCCACCCC ACCCCTTCCC TCTTCTGAAA GGCCTCTGTG GCCCCTCTGC CCCCCTTCCTG GCCCCACGAG AGTGGAGGGG GAGACTGTGC AGGGGGGAGC CATGGGCCCT	660 720
35	CAACCCCTCTC CCCAGAGCCT AGGGCCTGGC CTTTCCACTA CTGCAGGGCA CCGCAGTTCT GGGGGACGGT CCAGGGGGGG ACACAGGGCC TCCCTTTGGG GGCAGCTGCC CACCTCCTAC	780 840
	TTGCCTATCT ACACTCCCAA TGTGGTATG CCCCCTGSCAC CACCACCCAC CTCCGTGCC CAGTGTCCGT CAACCAGCCC TGCCTACTGG GGGGTGGCCC CTGAAACCCG AGGGCCCCCA	900 960
40	GGGCTGCTCT GCGATCTAAA CGCCCTCTTC CAAGGGTGC CACCAACAA AAGCATCTAC GACGTTTGGG TCAGCCACCC TCGGGACCTG GCGGCCCCCTG GCCCAGGCTG GCTGCTCTCC	1020 1080
	TGGTGCAGCC TGTGAGGCTC TTAAGACAGG GGCGCTCCT CCCCTCCGCT CCCACCCCCA CCTTGTGAC AGGGAGCCAA GGCGAGGCCG CTGTCCTGCGA CACAGCAGC CTCGAAACAC	1140 1200
	CAGGCAGCAG CCTTGCTGGG AGTCCACGGT GTTTATTGGG CCACCCCCACG CATGGCCGTG 45 GCCCAGCTGG GCACAAACCT CACCCCTGGTC TGTCACTGCCCT GTTTTTCCCTA CACTCAGCGG	1260 1320
	CAAAACTGCA GGAGCGAGGCT GAACCTGAAT ATCCCTTCCT AATCCCTCTT CTCAGCCCCAC TACCCATCCA TCAGTCACCA GCCGTCACCT CCCTCCCGTG CTCCAGCTGG GGGAAAGGAAA	1380 1440
	ACCCATGTGG ATCACCTGAA ATCCTGCCCT CTCTCTCTGT CGGAAAAGAA GTCCACCTTT	1500

TTCCGGAAAC CGGTTAGGGA ATTAAAATGC CCTACATGTC	CTGGTGGTTG	GGGGGGAAAC	1560
CACTAAAGGA ATTTGCAACC TTTTTTATCC TCTTCATTT	ATCCCAAGGG	GGGGCCCGTC	1620
CCATTTCCCC AACC			1634

(2) INFORMATION FOR SEQ ID NO:14:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 544 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:

(A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Human FAST-1

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Pro	Cys	Ser	Gly	Ser	Arg	Leu	Gly	Pro	Pro	Glu	Ala	Glu	Ser
1															15
Pro	Ser	Gln	Pro	Pro	Lys	Arg	Arg	Lys	Lys	Arg	Tyr	Leu	Arg	His	Asp
															20
Lys	Pro	Pro	Tyr	Thr	Tyr	Leu	Ala	Met	Ile	Ala	Leu	Val	Ile	Gln	Ala
															35
Ala	Pro	Ser	Arg	Arg	Leu	Lys	Leu	Ala	Gln	Ile	Ile	Arg	Gln	Val	Gln
															50
Ala	Val	Phe	Pro	Phe	Phe	Arg	Glu	Asp	Tyr	Glu	Gly	Trp	Lys	Asp	Ser
															65
Ile	Arg	His	Asn	Leu	Ser	Ser	Asn	Arg	Cys	Phe	Arg	Lys	Val	Pro	Lys
															85
Asp	Pro	Ala	Lys	Pro	Gln	Ala	Lys	Gly	Asn	Phe	Trp	Ala	Val	Asp	Val
															100
Ser	Leu	Ile	Pro	Ala	Glu	Ala	Leu	Arg	Leu	Gln	Asn	Thr	Ala	Leu	Cys
															115
Arg	Arg	Trp	Gln	Asn	Gly	Gly	Ala	Arg	Gly	Ala	Phe	Ala	Lys	Asp	Leu
															130
Gly	Pro	Tyr	Val	Leu	His	Gly	Arg	Pro	Tyr	Arg	Pro	Pro	Ser	Pro	Pro
															145
Pro	Pro	Pro	Ser	Glu	Gly	Phe	Ser	Ile	Lys	Ser	Leu	Leu	Arg	Arg	Ser
															165
Gly	Glu	Gly	Ala	Pro	Trp	Pro	Gly	Leu	Ala	Pro	Gln	Asn	Ser	Pro	Val
															180
Pro	Ala	Gly	Thr	Gly	Asn	Asn	Gly	Glu	Glu	Ala	Val	Pro	Thr	Pro	Pro
															195
Leu	Pro	Ser	Ser	Glu	Arg	Pro	Leu	Trp	Pro	Leu	Cys	Pro	Leu	Pro	Gly
															210
Pro	Thr	Arg	Val	Glu	Gly	Glu	Thr	Val	Gln	Gly	Gly	Ala	Met	Gly	Pro
															225
Gln	Pro	Ser	Pro	Gln	Ser	Leu	Gly	Pro	Gly	Leu	Ser	Thr	Thr	Ala	Gly
															245

His Arg Ser Ser Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser Leu
 260 265 270
 Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val
 275 280 285
 5 Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro Ser
 290 295 300
 Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro Pro
 305 310 315 320
 Gly Leu Leu Cys Asp Leu Asn Ala Leu Phe Gln Gly Val Pro Pro Asn
 10 325 330 335
 Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala
 340 345 350
 Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu Glx Gly Ser Glx
 355 360 365
 15 Asp Arg Gly Arg Ser Ser Leu Pro Leu Pro Pro Pro Cys Glx Gln
 370 375 380
 Gly Ala Lys Ala Arg Arg Leu Ser Ala Thr Thr Ala Ala Ser Lys His
 385 390 395 400
 Gln Ala Ala Ala Leu Leu Gly Val His Gly Val Tyr Trp Ala Thr Pro
 20 405 410 415
 Arg Met Ala Val Ala Gln Leu Gly Thr Thr Leu Thr Leu Val Cys His
 420 425 430
 Ala Cys Phe Ser Tyr Thr Gln Arg Gln Asn Cys Arg Ser Arg Leu Asn
 435 440 445
 25 Leu Asn Ile Pro Ser Glx Ser Leu Phe Ser Ala His Tyr Pro Ser Ile
 450 455 460
 Ser His Gln Pro Ser Pro Pro Ser Arg Ala Pro Ala Gly Gly Arg Lys
 465 470 475 480
 Thr His Val Asp His Leu Lys Ser Cys Pro Leu Ser Leu Ser Glu Lys
 30 485 490 495
 Lys Ser Thr Phe Phe Arg Lys Pro Val Arg Glu Leu Lys Cys Pro Thr
 500 505 510
 Cys Pro Gly Gly Trp Gly Gly Asn His Glx Arg Asn Leu Gln Pro Phe
 515 520 525
 35 Leu Ser Ser Phe Ile Tyr Pro Lys Gly Gly Pro Val Pro Phe Pro Gln
 530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other

- (B) LOCATION: 1...1

- (D) OTHER INFORMATION: Human FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gln Gly Gly Ala Met Gly Pro Gln Pro Ser Pro Gln Ser Leu Gly Pro
 1 5 10 15
 Gly Leu Ser Thr Thr Ala Gly His Arg Ser Ser Gly Gly Arg Ser Ser
 20 25 30
 5 Gly Gly His Arg Ala Ser Leu Trp Gly Gln Leu Pro Thr Ser Tyr Leu
 35 40 45
 Pro Ile Tyr Thr Pro Asn Val Val Met Pro Leu Ala Pro Pro Pro Thr
 50 55 60
 Ser Cys Pro Gln Cys Pro Ser Thr Ser Pro Ala Tyr Trp Gly Val Ala
 65 70 75 80
 10 Pro Glu Thr Arg Gly Pro Pro Gly Leu Leu Cys Asp Leu Asn Ala Leu
 85 90 95
 Phe Gln Gly Val Pro Pro Asn Lys Ser Ile Tyr Asp Val Trp Val Ser
 100 105 110
 15 His Pro Arg Asp Leu Ala Ala Pro Gly Pro Gly Trp Leu Leu Ser Trp
 115 120 125
 Cys Ser Leu Glx Gly Ser Glx Asp Arg Gly Arg Ser Ser Leu Pro Leu
 130 135 140
 Pro Pro Pro Pro Cys Glx Gln Gly Ala Lys Ala Arg Arg Leu Ser Ala
 145 150 155 160
 Thr Thr Ala Ala Ser Lys His Gln Ala Ala Leu Leu Gly Val His
 165 170 175
 Gly Val Tyr Trp Ala Thr Pro Arg Met Ala Val Ala Gln Leu Gly Thr
 180 185 190
 20 Thr Leu Thr Leu Val Cys His Ala Cys Phe Ser Tyr Thr Gln Arg Gln
 195 200 205
 Asn Cys Arg Ser Arg Leu Asn Leu Asn Ile Pro Ser Glx Ser Leu Phe
 210 215 220
 Ser Ala His Tyr Pro Ser Ile Ser His Gln Pro Ser Pro Pro Ser Arg
 225 230 235 240
 Ala Pro Ala Gly Gly Arg Lys Thr His Val Asp His Leu Lys Ser Cys
 245 250 255
 Pro Leu Ser Leu Ser Glu Lys Lys Ser Thr Phe Phe Arg Lys Pro Val
 260 265 270
 25 Arg Glu Leu Lys Cys Pro Thr Cys Pro Gly Gly Trp Gly Gly Asn His
 275 280 285
 Glx Arg Asn Leu Gln Pro Phe Leu Ser Ser Phe Ile Tyr Pro Lys Gly
 290 295 300
 40 Gly Pro Val Pro Phe Pro Gln
 305 310

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other

- (B) LOCATION: 1...1

(D) OTHER INFORMATION: Mouse FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5	ATGGCCTCG GCTGGGACCT GGCCTCAACT TACACTCCGA CTACCCGAG CCCCCAGTTA GCCCTGGCTC CGGCCCAGGG CTACCTCCCT TGTATGGGGC CTCGCGACAA CTCTCAGCTG	60 120
	AGGCCTCCAG AGGCAGAGTC TCTTCGAAG ACCCCCAAGA GGAGGAAGAA GAGATACTA CGGCATGACA AGCCCCCTA CACCTACTTG GCCATGATCG CCTTGGTAAT TCAGGCGCA	180 240
10	CCCTTCCGCA GGCTGAAACT GGCTCAGGTC CAGGCAGTGT TCCCCCTCTT CAGGGACGAC TATGAGGGCT GGAAGGACTC CATCCGCCAC AACCTTCCT CTAATCGGTG CTTCCATAAG	300 360
	GTGCCAAGG ACCCTGCAAA GCCCCAGGC AAGGGCAACT TCTGGCGGT GGATGTTAGC CTGATTCCCTG CTGAGGCAGCT GCGCCITTCAG AACACTGCC C TGTGGCGTCG ATGGCAGAAC	420 480
	CGGGGCACCC ACAGAGCTT CGCCAAGGAC CTGAGCCCT ACGTGCTCCA CGGCCAGCCT TATCAGGCCAC CCAGTCCCCC ACCACCACCT AGGGAGGGTT TCAGGCATCAA GTCCCTGCTA	540 600
15	GGGGACCTG GGAAAGAATC CACATGGCC CAGCATCTG GGCTCCCTGG ACAGAGCACT GCAGCTCAGG CAGGCACCTT GTCAAAGGGG GAAGAAGGGG TGGGACTGG ACCCTCTAGC	660 720
	TCCTCTGAGA CGCCTCTGTG GCCCCCTGTG TCCCCTCTG GGCCCACAAT CATAGAGGG GAGAGTCCC AAGGGGAGGT AATCAGGCCT TCTCCGTCA CCCCAGATCA AGGCTCCTGG	780 840
20	CCCCCTCCACT TACTTGAGGA TTCCGAGAT TCCAGGGAG TGCCCAGGAG GGGGAGCAGA GCCTCCTTGT GGGGACAGCT ACCCACTTCT TACTTGCCA TCTATACGCC CAATGTAGTA ATGCCCTTGG CCACACTACC GACCACCTCT TGTCCCCAGT GCCCATCTTC TGCCAGGCCA	900 960 1020
	GCTTACTGGA GCGTAGGCAC TGAATCCAA GGGTCCCAGG ACCTGCTCTG TGATCTAGAC TCCCTCTTCC AGGGAGTACC ACCAACAAAG AGTATCTATG ATGTGTGGGT CAGCCATCCT	1080 1140
25	AGGGACCTGG CAGCTCCTGC CCCAGGCTGG CTCCCTTCTT GGTACAGCAT GTAATATTCT AGGGCAGAAA GGGCTGTTCT CTCTTCCACC CATGAATATC ATTTTGATGA ACCAGAGCTA GGACGATGTC CCGACGGACA GCTTTAAAC ACCAGCACAG CTTGCTGAA AACCCACAGC	1200 1260 1320
	TTTAATTAGG TTACTCCAGA AAGGGTTGTC TCTGCTAGAT AGGGAGGTCT GGCCAATCGT GCCAGGAGCG GAGCTCAGCC TGTAGAGTGC CTCCCTTGA TCCTACCTTT TCAGGCCCTC	1380 1440
30	AAGCCATCCA TCTATCCATC CCTCTGTCA CATGCCCTCC TGGCTCCAGG CTGGGGGGAG GGAGAGCCAA AAGTGGGTCT GATCTGAAGT CTTGCCCTCT CTCAAATGCC TGGGTAGAGG GTAGCACCTT TCAGGGAAAG GGTAAAGAAA TGAAAGACTG GAACGGACAT AATTTTGGTG	1500 1560 1620
	TAATGGAAGT AGGGGAGCGA TTAATAGTAA AGGAATTAC AACATTAA	1668

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Mouse FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

45	Met Ala Ser Gly Trp Asp Leu Ala Ser Thr Tyr Thr Pro Thr Thr Pro	
	1 5 10 15	

Ser Pro Gln Leu Ala Leu Ala Pro Ala Gln Gly Tyr Leu Pro Cys Met
 20 25 30
 Gly Pro Arg Asp Asn Ser Gln Leu Arg Pro Pro Glu Ala Glu Ser Leu
 35 40 45
 5 Ser Lys Thr Pro Lys Arg Arg Lys Lys Arg Tyr Leu Arg His Asp Lys
 50 55 60
 Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala Ala
 65 70 75 80
 Pro Phe Arg Arg Leu Lys Leu Ala Gln Val Gln Ala Val Phe Pro Phe
 10 Phe Arg Asp Asp Tyr Glu Gly Trp Lys Asp Ser Ile Arg His Asn Leu
 85 90 95
 Ser Ser Asn Arg Cys Phe His Lys Val Pro Lys Asp Pro Ala Lys Pro
 115 120 125
 15 Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val Ser Leu Ile Pro Ala
 130 135 140
 Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys Arg Arg Trp Gln Asn
 145 150 155 160
 Arg Gly Thr His Arg Ala Phe Ala Lys Asp Leu Ser Pro Tyr Val Leu
 20 His Gly Gln Pro Tyr Gln Pro Pro Ser Pro Pro Pro Pro Arg Glu
 180 185 190
 Gly Phe Ser Ile Lys Ser Leu Leu Gly Asp Pro Gly Lys Glu Ser Thr
 195 200 205
 25 Trp Pro Gln His Pro Gly Leu Pro Gly Gln Ser Thr Ala Ala Gln Ala
 210 215 220
 Gly Thr Leu Ser Lys Gly Glu Glu Gly Met Gly Thr Gly Pro Ser Ser
 225 230 235 240
 Ser Ser Glu Thr Pro Leu Trp Pro Leu Cys Ser Leu Pro Gly Pro Thr
 245 250 255
 30 Ile Ile Glu Gly Glu Ser Ser Gln Gly Glu Val Ile Arg Pro Ser Pro
 260 265 270
 Val Thr Pro Asp Gln Gly Ser Trp Pro Leu His Leu Leu Glu Asp Ser
 275 280 285
 35 Ala Asp Ser Arg Gly Val Pro Arg Arg Gly Ser Arg Ala Ser Leu Trp
 290 295 300
 Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val
 305 310 315 320
 Met Pro Leu Ala Thr Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser
 40 Met Pro Leu Ala Thr Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser
 325 330 335
 Ser Ala Ser Pro Ala Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser
 340 345 350
 Gln Asp Leu Leu Cys Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro
 355 360 365
 45 Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala
 370 375 380
 Ala Pro Ala Pro Gly Trp Leu Leu Ser Trp Tyr Ser Met
 385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

5 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Mouse FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10 Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val Met Pro Leu Ala Thr
1 5 10 15
Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser Ser Ala Ser Pro Ala
20 25 30
Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser Gln Asp Leu Leu Cys
35 40 45
Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro Asn Lys Ser Ile Tyr
50 55 60
Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala Pro Ala Pro Gly
65 70 75 80
Trp Leu Leu Ser Trp Tyr Ser Met
85